

RESULT 1  
US-09-745-763-35  
Sequence 35, Application US/09745763  
Patent No. US20020065394A1  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
McCoy, John M.  
Lavallee, Edward R.  
Collins-Racie, Lisa A.  
Evans, Cheryl  
Merberg, David  
Treacy, Maurice  
Spaulding, Vikki  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
ENCODING THEM  
NUMBER OF SEQUENCES: 219  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark Drive  
CITY: Cambridge  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02140

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/745,763  
 FILING DATE: 18-Jun-2000  
 CLASSIFICATION: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sprunger, Suzanne A.  
 REGISTRATION NUMBER: 41,323  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 498-8284  
 TELEFAX: (617) 876-5851  
 INFORMATION FOR SEQ ID NO: 35:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1851 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
 US-09-745-763-35  
 Alignment Scores:  
 Pred. No.: 3,72e-289 Length: 1851  
 Score: 2417.00 Matches: 472  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-745-763-36 (1-472) x US-09-745-763-35 (1-1851)  
 QY 1 MetLysPheLeuIlePheAlaPhePheGlyValAlaIleuLeuSerLeuCySerGly 20  
 DB 99 ATGAATTCCTATCTTGSCATTTTCGGTGTGTCACCTTTATCCCTGTCCTGG 158  
 QY 21 LysAlaIleCyLysAsnGlyIleSerLysArgThrPheGluIleLysGluIle 40  
 DB 159 AAAGCTATATGCAAGATGGCATCTCTAAGAGCACTTTTGAAGAAATTAAGAAATA 218  
 QY 41 AlaSerCySGlyAspValAlaLysAlaIleIleAsnLeuAlaValIleGlyLysAlaGln 60  
 DB 219 GCCAGCTGTGAGATGTGCTTAAGCAATCATCAACCTAGCTTTATGTGTAAGCCAG 278  
 QY 61 AsnArgSerIleGluArgLeuAlaLeuLeuValAspThrValGlyProArgLeuSerGly 80  
 DB 279 AACAGATCTTATGAGCATGGCACTTCTGTTGATCTGTTGACCCAGCTGAGTGGC 338  
 QY 81 SerLysAsnLeuGluLysAlaIleGlnIleMetIleAsnLeuGlnIleAspGlyLeu 100  
 DB 339 TCCAGAGACCTTAAGAAAGCCATCCAAATTAATGTACCAAACTGGACAGCAAGTGGG 398  
 QY 101 GluLysValHisLeuGluProValArgIleProHisTrpGluArgGlyGluGluSerAla 120  
 DB 399 GAGAAAGTTCACCTGGAGCCAGTGAATACCCCACTGGAGAGGGAGAAATCAGCT 458  
 QY 121 ValMetLeuGluProArgIleHisLysIleAlaIleLeuGlyLeuGlySerSerIleGly 140  
 DB 459 GTGATGCTGAGCAAGAAATTCATTAAGTACCATCTGGGCTTTGGACAGCAATGGG 518  
 QY 141 ThrProProGluGlyIleThrAlaGluValLeuValIleThrSerPheAspGluLeuGln 160  
 DB 519 ACTCCTCCAGAAAGCATTAACAGCAAGTCTGGGTGAGCCTCTTCGATGAATCGAG 578  
 QY 161 ArgArgLysSerGluAlaArgGlyLysIleValIleValIleArgGlnProGlyIleAsnTyr 180  
 DB 579 AGAAGGCGCTTAAGAGCAAGAGGAGATGTGTATTATTAACCAACCTTACATCACTAC 638  
 QY 181 SerArgThrValGlnTyrArgThrGlnGlyValAlaGluAlaLysValIleValAlaLeu 200

DB 639 TCAGAGCGGTGCAATACCGAAGCGAGGGCGGTGGAAGCTGCCAAGGTGGGGCTTTG 698  
 QY 201 AlaSerLeuIleArgSerValAlaSerPheSerIleTyrSerProHisThrGlyIleGln 220  
 DB 699 GCATCTTCATTCATCCGTGGGCTCTCTCCATCTCAACATCTCTCCACAGGATTTGAG 758  
 QY 221 GluTyrGlnAspGlyValProLysIleProThrAlaCysIleThrValGluAspAlaGlu 240  
 DB 759 GAATACCAAGATGGCGTGGCCCAAAATTCACACAGCTGTATTACGTGGAGAACAGAA 818  
 QY 241 MetMetSerArgMetAlaSerHisGlyIleLysIleValIleGlnLeuLysMetGlyAla 260  
 DB 819 ATGATGTCAAGAAATGCTTCTTCATGGATCAAAATTCATTCAGCTTAAGATGGGGCA 878  
 QY 261 LysThrTyrProAspThrAspSerPheAsnThrValAlaGluIleThrGlySerLysTyr 280  
 DB 879 AAGACCTAACCCAGATGATGATCTCTTCAACACCTGACAGAGATCACTGGAGCAAAATAT 938  
 QY 281 ProGluGlnValValLeuValSerGlyHisLeuAspSerTrpAspValGlyGlnGlyAla 300  
 DB 939 CCAGAACAGGTGTGATCGTTCAGTGCACATCTGCACAGCTGGAGATGTGGCAGAGTGC 998  
 QY 301 MetAspAspGlyGlyGlyAlaPheIleSerTrpGluAlaLeuSerLeuIleLysAspLeu 320  
 DB 999 ATGATGATGCGCGGTGAGCCTTTATATCATGGAGACACTCTCATTTATTAAGATCTT 1058  
 QY 321 GlyLeuArgProLysArgThrLeuArgLeuValLeuThrArgIleGluGlnGlyGly 340  
 DB 1059 GGGGTGCTCCAAAGAGCACTTGGCGCTGTGTCTGCACTGCAAGAGAAACAAGTGA 1118  
 QY 341 ValGlyAlaPheGlnTyrTyrGlnLeuHisLysValAsnIleSerAsnTyrSerLeuVal 360  
 DB 1119 GTTGTCCTTCCAGATTAATCAATTACCAAGGTAATTTTCCAACTACAGCTGGTG 1178  
 QY 361 MetGluSerAspAlaGlyThrPheLeuProThrGlyLeuGlnPheThrGlySerGlyLys 380  
 DB 1179 ATGAGGCTGACCAAGCAAGAACCTTCTTACCACTGGCGCTGCAAATTCACCTGGCAAGAAAG 1238  
 QY 381 AlaArgAlaIleMetGluGluValMetSerLeuLeuGlnProLeuAsnIleThrGlnVal 400  
 DB 1239 GCCAGGCGCATCATGAGAGGTTATGAGCTCTGTCAGCCCTCATATATCATCAAGGTC 1298  
 QY 401 LeuSerHisGlyGluGlyThrAspIleAsnPheTrpIleGlnAlaGlyValProGlyAla 420  
 DB 1299 CTGAGCCATGGAAGAGAGCAAGCATCACTTTTGGATCCAACTGTGAGTGGCTCGAGCC 1358  
 QY 421 SerLeuLeuAspAspLeuTyrLysTyrPhePhePheHisSerHisGlyAspThrMet 440  
 DB 1359 AGTCTACTGATGACTTATACAGATATTTCTTCTTCATCATCACTCCACGAGACACCATG 1418  
 QY 441 ThrValMetAspProLysGlnMetAsnValAlaAlaAlaValThrAlaValValSerTyr 460  
 DB 1419 ACTGTATGATTCCAAGACAGATGAATGTTGCTGCGCTGTGGCTGTGGCTGTGTTCTTAT 1478  
 QY 461 ValValAlaAspMetGluGluMetLeuProArgSer 472  
 DB 1479 GTTGTTCAGACATGGAAGAAATGCTGCTAGGTCC 1514